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RAW SEQUENCE LISTING

DATE: 03/25/2002

PATENT APPLICATION: US/09/810,927B

TIME: 15:45:34

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03222002\I810927B.raw

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4 <110> APPLICANT: Jing, Shuqian
6 <120> TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
8 <130> FILE REFERENCE: 01017/36917A
10 <140> CURRENT APPLICATION NUMBER: US 09/810,927B
11 <141> CURRENT FILING DATE: 2001-03-16
13 <150> PRIOR APPLICATION NUMBER: US 60/266,159
14 <151> PRIOR FILING DATE: 2001-02-02
16 <150> PRIOR APPLICATION NUMBER: US 09/723,232
17 <151> PRIOR FILING DATE: 2000-11-27
19 <150> PRIOR APPLICATION NUMBER: US 60/204,208
20 <151> PRIOR FILING DATE: 2000-05-12
22 <150> PRIOR APPLICATION NUMBER: US 60/189,923
23 <151> PRIOR FILING DATE: 2000-03-08
25 <160> NUMBER OF SEQ ID NOS: 27
27 <170> SOFTWARE: PatentIn Ver. 2.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1841
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
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35 <221> NAME/KEY: CDS
36 <222> LOCATION: (50)..(1555)
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41                                     1
43 gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
44 Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
45      5              10              15
47 ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
48 Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
49 20              25              30              35
51 cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
52 Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
53      40              45              50
55 cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
56 Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
57      55              60              65
59 gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
60 Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
61      70              75              80
64 acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346
65 Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys

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68	gtg agg tgc aat tac aca gag gcc ttc cag act cag acc aga ccc tct	394		
69	Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser			
70	100 105 110 115			
72	ggt ggt aaa tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac	442		
73	Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn			
74	120 125 130			
76	aca gtc tat ttc att ggg gcc cat aat att cct aat gca aat atg aat	490		
77	Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn			
78	135 140 145			
80	gaa gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta	538		
81	Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu			
82	150 155 160			
84	gac cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg	586		
85	Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu			
86	165 170 175			
88	tgg gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa	634		
89	Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu			
90	180 185 190 195			
92	gtg aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc	682		
93	Val Asn Phe Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile			
94	200 205 210			
96	caa cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag	730		
97	Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln			
98	215 220 225			
100	aag aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt	778		
101	Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser			
102	230 235 240			
104	gaa ggt gct acg gtg cag ctg act cca tat ttt cct act tgt ggc agc	826		
105	Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser			
106	245 250 255			
108	gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc cca caa aca ggc	874		
109	Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly			
110	260 265 270 275			
112	gtc cct ttc cct ctg gat aac aac aaa agc aag ccg gga ggc tgg ctg	922		
113	Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu			
114	280 285 290			
116	cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg gtg ctg gtg gca	970		
117	Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala			
118	295 300 305			
120	ggg atc tat cta atg tgg agg cac gaa agg atc aag aag act tcc ttt	1018		
121	Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe			
122	310 315 320			
124	tct acc acc aca cta ctg ccc ccc att aag gtt ctt gtg gtt tac cca	1066		
125	Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro			
126	325 330 335			
128	tct gaa ata tgt ttc cat cac aca att tgt tac ttc act gaa ttt ctt	1114		
129	Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu			
130	340 345 350 355			

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132 caa aac cat tgc aga agt gag gtc atc ctc gaa aag tgg cag aaa aag 1162
133 Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys
134 360 365 370
136 aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc act caa aag aag 1210
137 Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys
138 375 380 385
140 gca gca gac aaa gtc gtc ttc ctt tcc aat gac gtc aac agt gtg 1258
141 Ala Ala Asp Lys Val Val Phe Leu Ser Asn Asp Val Asn Ser Val
142 390 395 400
144 tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc agt gag aac tct 1306
145 Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
146 405 410 415
148 caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc agt gat cta aga 1354
149 Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
150 420 425 430 435
152 agc cag att cat ctg cac aaa tac gtg gtg gtc tac ttt aga gag att 1402
153 Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
154 440 445 450
156 gat aca aaa gac gat tac aat gct ctc agt gtc tgc ccc aag tac cac 1450
157 Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
158 455 460 465
160 ctc atg aag gat gcc act gct ttc tgt gca gaa ctt ctc cat gtc aag 1498
161 Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys
162 470 475 480
164 cag cag gtg tca gca gga aaa aga tca caa gcc tgc cac gat ggc tgc 1546
165 Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys
166 485 490 495
168 tgc tcc ttg tagccccaccc atgagaagca agagacotta aaggcttcc 1595
169 Cys Ser Leu
170 500
172 atccccaccaa ttacagggaa aaaacgtgtg atgatcctga agcttactat gcagcctaca 1655
174 aacagcotta gtaattaaaa cattttatac caataaaatt ttcaaataatt gctaactaat 1715
176 gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt tatacataga 1775
178 aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca ataaagcatc 1835
180 ttcagc 1841
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 502
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
188 <400> SEQUENCE: 2
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190 1 5 10 15
192 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
193 20 25 30
195 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
196 35 40 45
199 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
200 50 55 60
202 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu

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205	Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser	
206					85					90						95	
208	Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	Glu	Ala	Phe	Gln	Thr	Gln	Thr	
209				100					105						110		
211	Arg	Pro	Ser	Gly	Gly	Lys	Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	
212			115					120					125				
214	Glu	Leu	Asn	Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	
215		130					135					140					
217	Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	
218	145					150					155					160	
220	Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	
221				165						170					175		
223	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	
224				180					185					190			
226	Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	
227			195					200					205				
229	Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	
230		210					215					220					
232	Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	
233	225					230					235					240	
235	Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	
236				245						250					255		
238	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	
239				260					265					270			
241	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	
242			275				280					285					
244	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val	Ala	Thr	Trp	Val	
245		290					295					300					
247	Leu	Val	Ala	Gly	Ile	Tyr	Leu	Met	Trp	Arg	His	Glu	Arg	Ile	Lys	Lys	
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250	Thr	Ser	Phe	Ser	Thr	Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	Val	
251				325						330					335		
253	Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	Thr	
254				340					345				350				
256	Glu	Phe	Leu	Gln	Asn	His	Cys	Arg	Ser	Glu	Val	Ile	Leu	Glu	Lys	Trp	
257			355					360				365					
259	Gln	Lys	Lys	Lys	Ile	Ala	Glu	Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	Thr	
260		370					375					380					
262	Gln	Lys	Lys	Ala	Ala	Asp	Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	Val	
263	385					390					395					400	
265	Asn	Ser	Val	Cys	Asp	Gly	Thr	Cys	Gly	Lys	Ser	Glu	Gly	Ser	Pro	Ser	
266				405						410				415			
268	Glu	Asn	Ser	Gln	Asp	Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	
269			420						425				430				
271	Asp	Leu	Arg	Ser	Gln	Ile	His	Leu	His	Lys	Tyr	Val	Val	Val	Tyr	Phe	
272			435					440					445				
274	Arg	Glu	Ile	Asp	Thr	Lys	Asp	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro	
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277 Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
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281                      485                      490                      495
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284                      500
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288 <211> LENGTH: 539
289 <212> TYPE: PRT
290 <213> ORGANISM: Homo sapiens
292 <400> SEQUENCE: 3
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297                      20                      25                      30
299 Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln Pro Gly Leu
300                      35                      40                      45
302 Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
303                      50                      55                      60
305 Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu
306 65                      70                      75                      80
308 His Phe Ala His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile
309                      85                      90                      95
311 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
312                      100                     105                     110
314 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg
315                      115                     120                     125
317 Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Arg Trp Arg Thr
318                      130                     135                     140
320 Pro Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr Val Glu
321 145                     150                     155                     160
323 Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp Asn Glu
324                      165                     170                     175
326 Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met Glu Asn
327                      180                     185                     190
329 His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro Arg Pro Glu
330                      195                     200                     205
332 Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu Arg Asn Leu Lys
333                      210                     215                     220
335 Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser Ser Cys
336 225                     230                     235                     240
338 Leu Asn Asp Cys Leu Arg His Ser Ala Thr Val Ser Cys Pro Glu Met
339                      245                     250                     255
341 Pro Asp Thr Pro Glu Pro Ile Pro Asp Tyr Met Pro Leu Trp Val Tyr
342                      260                     265                     270
344 Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val Ile Leu
345                      275                     280                     285
347 Leu Ile Val Cys Met Thr Trp Arg Leu Ala Gly Pro Gly Ser Glu Lys
348                      290                     295                     300

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VERIFICATION SUMMARY

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